

## FIG. 1A

5'                   11                   20                   29                   38                   47                   56  
 GAG ACT CAC GGT CAA GCT AAG GCG AAG AGT GGG TGG CTG AAG CCA TAC TAT TTT  
 -----  
                   65                   74                   83                   92                   101                   110  
 ATA GAA TTA ATG GAA AGC AGA AAA GAC ATC ACA AAC CAA GAA GAA CTT TGG AAA  
 -----  
                   M   E   S   R   K   D   I   T   N   Q   E   E   L   W   K  
 -----  
                   119                   128                   137                   146                   155                   164  
 ATG AAG CCT AGG AGA AAT TTA GAA GAA GAC GAT TAT TTG CAT AAG GAC ACG GGA  
 -----  
 M   K   P   R   R   N   L   E   E   D   D   Y   L   H   K   D   T   G  
 -----  
                   173                   182                   191                   200                   209                   218  
 GAG ACC AGC ATG CTA AAA AGA CCT GTG CTT TTG CAT TTG CAC CAA ACA GCC CAT  
 -----  
 E   T   S   M   L   K   R   P   V   L   L   H   L   H   Q   T   A   H  
 -----  
                   227                   236                   245                   254                   263                   272  
 GCT GAT GAA TTT GAC TGC CCT TCA GAA CTT CAG CAC ACA CAG GAA CTC TTT CCA  
 -----  
 A   D   E   F   D   C   P   S   E   L   Q   H   T   Q   E   L   F   P  
 -----  
                   281                   290                   299                   308                   317                   326  
 CAG TGG CAC TTG CCA ATT AAA ATA GCT GCT ATT ATA GCA TCT CTG ACT TTT CTT  
 -----  
 Q   W   H   L   P   I   K   I   A   A   I   I   A   S   L   T   F   L  
 -----  
                   335                   344                   353                   362                   371                   380  
 TAC ACT CTT CTG AGG GAA GTA ATT CAC CCT TTA GCA ACT TCC CAT CAA CAA TAT  
 -----  
 Y   T   L   L   R   E   V   I   H   P   L   A   T   S   H   Q   Q   Y  
 -----  
                   389                   398                   407                   416                   425                   434  
 TTT TAT AAA ATT CCA ATC CTG GTC ATC AAC AAA GTC TTG CCA ATG GTT TCC ATC  
 -----  
 F   Y   K   I   P   I   L   V   I   N   K   V   L   P   M   V   S   I  
 -----  
                   443                   452                   461                   470                   479                   488  
 ACT CTC TTG GCA TTG GTT TAC CTG CCA GGT GTG ATA GCA GCA ATT GTC CAA CTT  
 -----  
 T   L   L   A   L   V   Y   L   P   G   V   I   A   A   I   V   Q   L  
 -----  
                   497                   506                   515                   524                   533                   542  
 CAT AAT GGA ACC AAG TAT AAG AAG TTT CCA CAT TGG TTG GAT AAG TGG ATG TTA  
 -----  
 H   N   G   T   K   Y   K   K   F   P   H   W   L   D   K   W   M   L  
 -----  
                   551                   560                   569                   578                   587                   596  
 ACA AGA AAG CAG TTT GGG CTT CTC AGT TTC TTT TTT GCT GTA CTG CAT GCA ATT  
 -----  
 T   R   K   Q   F   G   L   L   S   F   F   F   A   V   L   H   A   I  
 -----  
                   605                   614                   623                   632                   641                   650  
 TAT AGT CTG TCT TAC CCA ATG AGG CGA TCC TAC AGA TAC AAG TTG CTA AAC TGG  
 -----  
 Y   S   L   S   Y   P   M   R   R   S   Y   R   Y   K   L   L   N   W  
 -----

184 185

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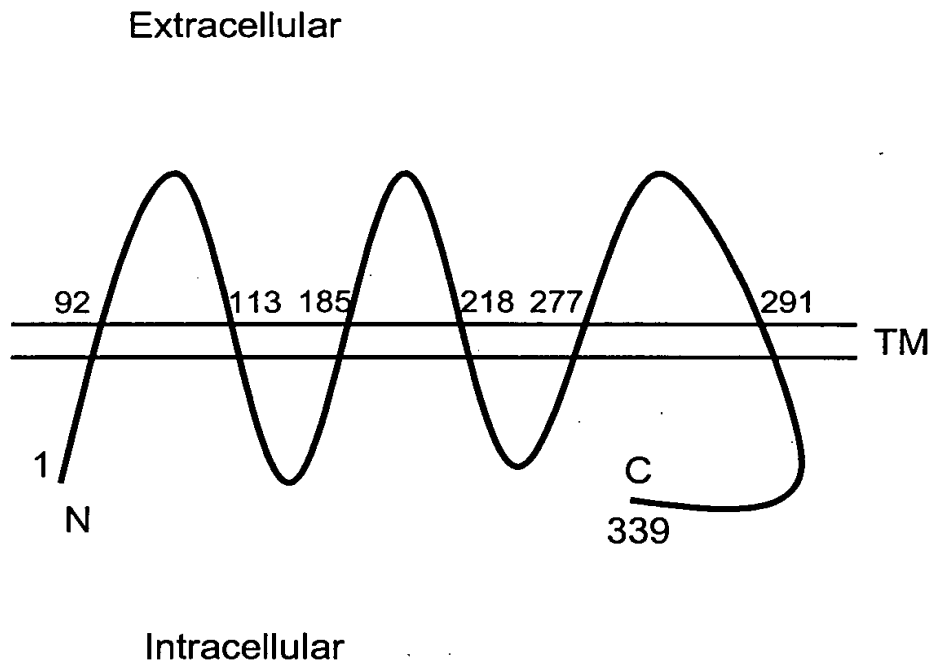
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 A Y Q Q V Q Q N K E D A W I E H D V  
 713 722 731 740 749 758  
 TGG AGA ATG GAG ATT TAT GTG TCT CTG GGA ATT GTG GGA TTG GCA ATA CTG GCT  
 W R M E I Y V S L G I V G L A I L A  
 767 776 785 794 803 812  
 CTG TTG GCT GTG ACA TCT ATT CCA TCT GTG AGT GAC TCT TTG ACA TGG AGA GAA  
 L L A V T S I P S V S D S L T W R E  
 821 830 839 848 857 866  
 TTT CAC TAT ATT CAG AGC AAG CTA GGA ATT GTT TCC CTT CTA CTG GGC ACA ATA  
 F H Y I O S K L G I V S L L L G T I  
 875 884 893 902 911 920  
 CAC GCA TTG ATT TTT GCC TGG AAT AAG TGG ATA GAT ATA AAA CAA TTT GTA TGG  
 H A L I F A W N K W I D I K Q F V W  
 929 938 947 956 965 974  
 TAT ACA CCT CCA ACT TTT ATG ATA GCT GTT TTC CTT CCA ATT GTT GTC CTG ATA  
 Y T P P T F M I A V F L P I V V L I  
 983 992 1001 1010 1019 1028  
 TTT AAA AGC ATA CTA TTC CTG CCA TGC TTG AGG AAG AAG ATA CTG AAG ATT AGA  
 F K S I L F L P C L R K K I L K I R  
 1037 1046 1055 1064 1073 1082  
 CAT GGT TGG GAA GAC GTC ACC AAA ATT AAC AAA ACT GAG ATA TGT TCC CAG TTG  
 H G W E D V T K I N K T E I C S Q L  
 1091 1100 1109 1118 1127 1136  
 TAG AAT TAC TGT TTA CAC ACA TTT TTG TTC AAT ATT GAT ATA TTT TAT CAC CAA  
 \* N Y C L H T F L F N I D I F Y H Q  
 1145 1154 1163 1172 1181 1190  
 CAT TTC AAG TTT GTA TTT GTT AAT AAA ATG ATT ATT CAA GGA AAA AAA AAA AAA  
 H F K F V F V N K M I I Q G K K K K

AAA AA 3'

K

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FIG. 1B



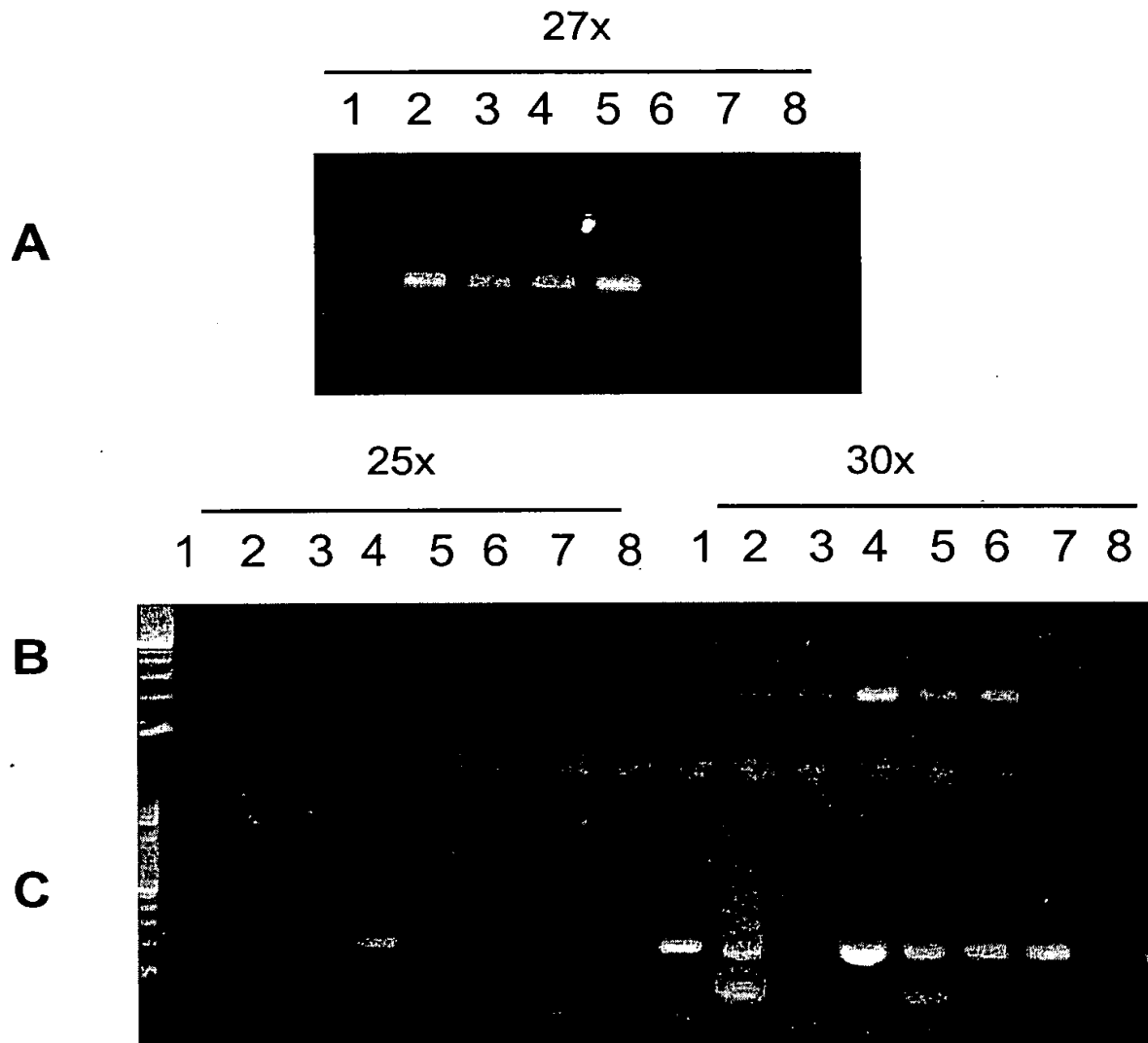
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# FIG. 1C

5' GGC GGA GGC GGA GGC GGA GGG CGA GGG GCG GGG AGC GCC GCC TGG AGC GCG  
GCA GGT CAT ATT GAA CAT TCC AGA TAC CTA TCA TTA CTC GAT GCT GTT GAT  
AAC AGC AAG 3'

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**FIG. 2**



**Panels:**

**A**

1. Brain
2. Prostate
3. LAPC-4 AD
4. LAPC-4 AI
5. LAPC-9 AD
6. HeLa
7. Murine cDNA
8. Neg. control

**B**

1. Brain
2. Heart
3. Kidney
4. Liver
5. Lung
6. Pancreas
7. Placenta
8. Skeletal Muscle

**C**

1. Colon
2. Ovary
3. Leukocytes
4. Prostate
5. Small Intestine
6. Spleen
7. Testis
8. Thymus

FIG. 3A

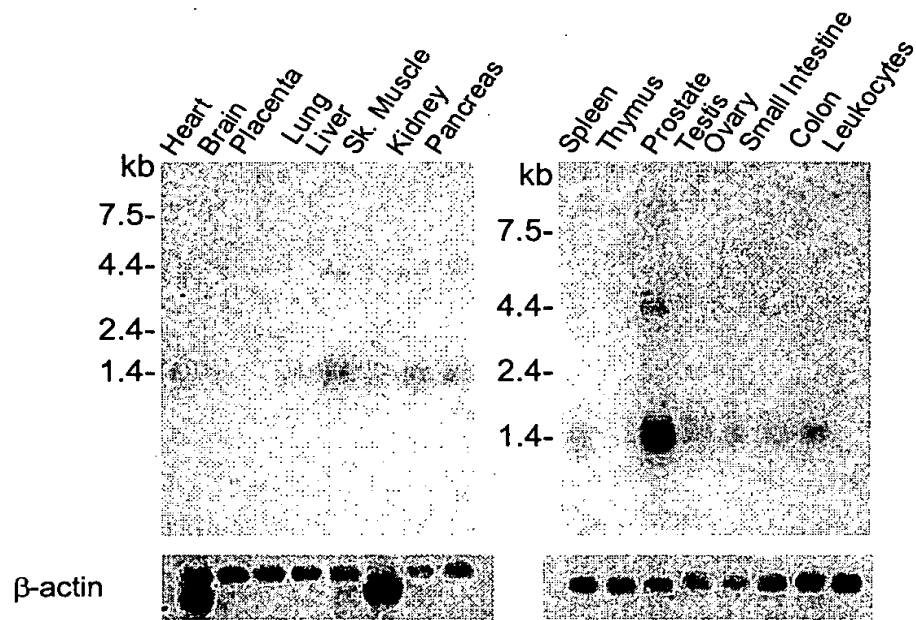
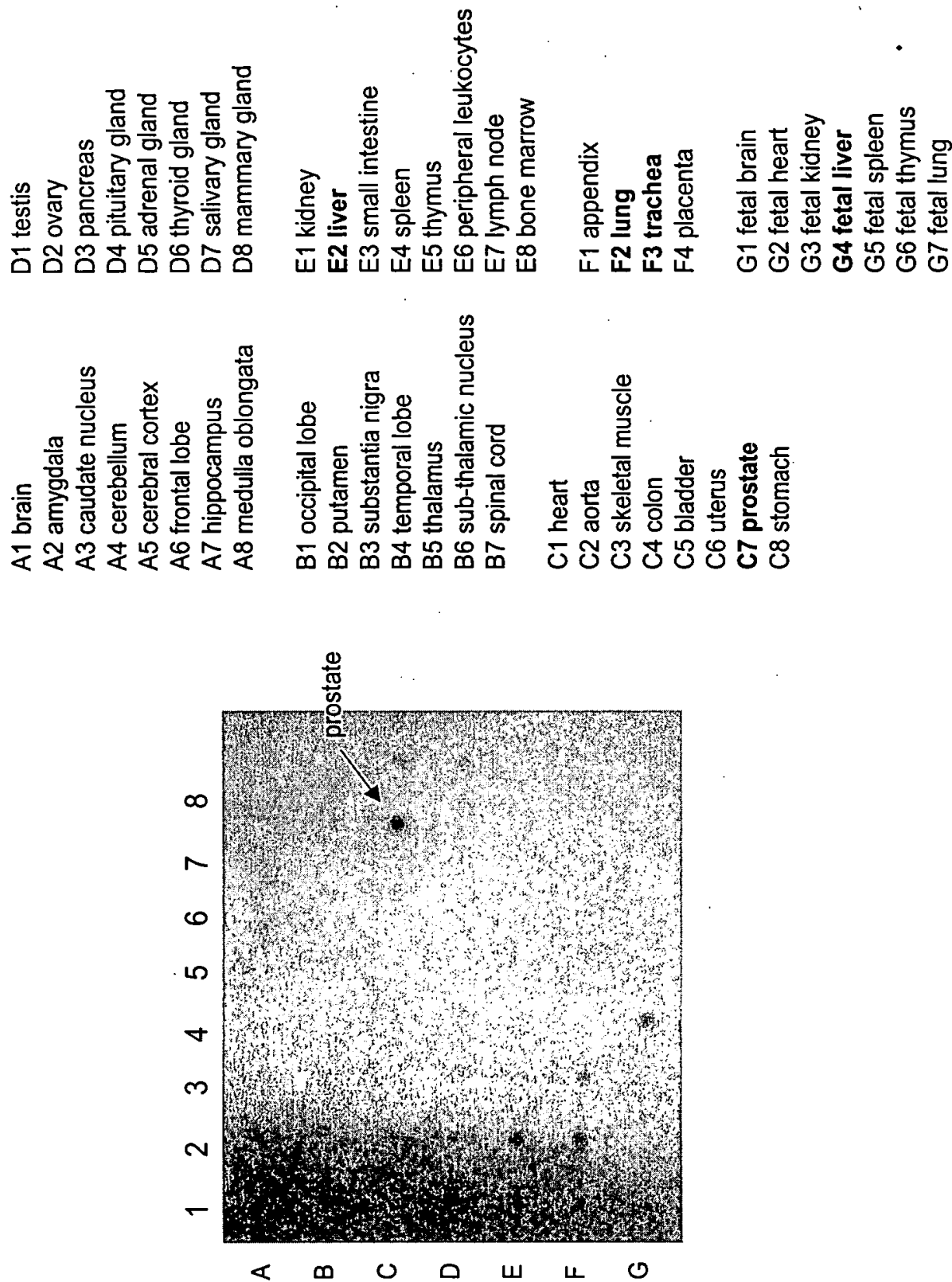


FIG. 3B



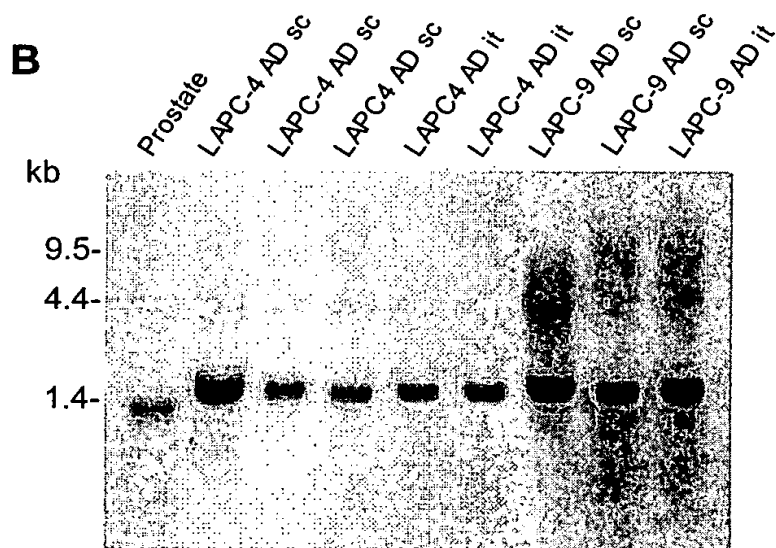
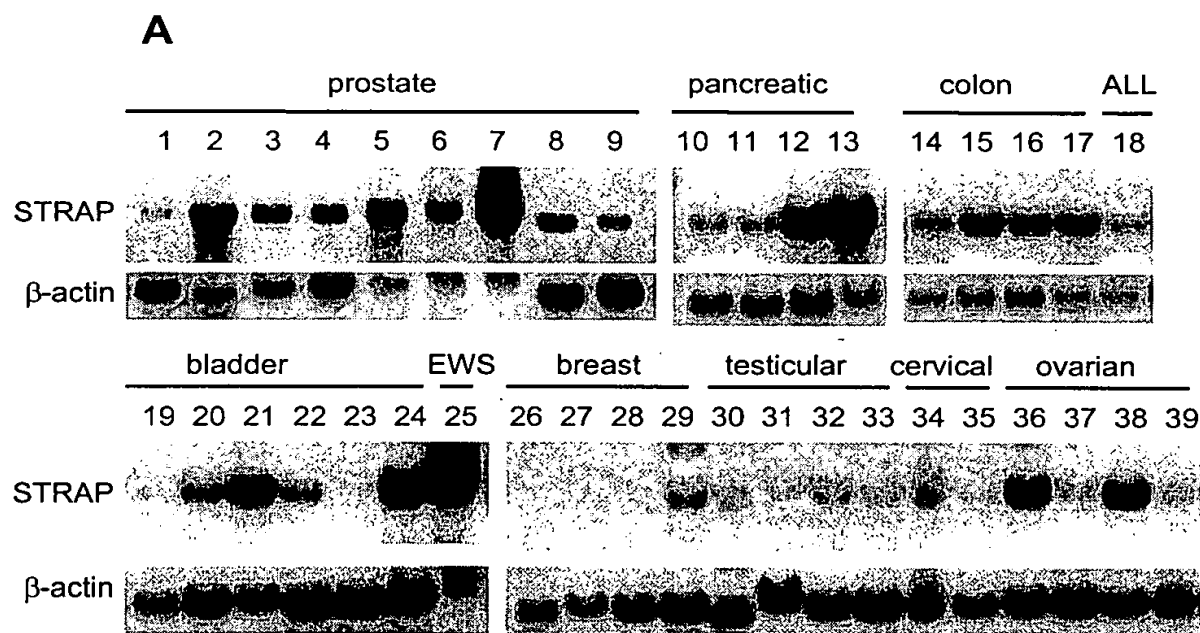
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AGAAATTTAGAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGC  
ATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACTCTTTCACA  
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CACCCCTTAGCAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGG  
TTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACCTTCATAATGGAACCAA  
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ATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTGTCTCT  
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AGAGAATTTCACTATATTCAGGTAATAATATATAAAATAACCCTAAGAGGTAAATCTTCTTTTGTGTTTATGAT  
ATAGAATATGTTGACTTTACCCCATAAAAATAACAAATGTTTTTCAACAGCAAAGATCTTATACTTGTTCCAATT  
AATAATGTGCTCTCCTGTTGTTTTCCCTATTGCTTCTAATTAGGACAAGTGTTTCCTAGACATAAATAAAGGCAT  
TAAAAATATTCTTTGTTTTTTTTTTTTTGTGTTGTTGTTTTTTGTTGTTGTTGTTGTTTTTTTGAGATGAAGTCTCG  
CTCTGTTGCCCATGCTGGAGTACAGTGGCACGATCTCGGCTCACTGCAACCTGCGCCTCCTGGGTTTCAGGCGATT  
TCTTGCCCTCAGCCTCCTGAGTAGCTGGGATTACAGGCACCCATCACCATGTCCAGCTAATTTTGTATTTTATGTA  
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AAAGTGCTGGGATGACAGTTGTGAGCCACCACACTCAGCCTGCTCTTCTAATATTGAAACTTGTTAGACAATTT  
GCTACCCATCTAATGTGATATTTTAGGAATCCAATATGCATGGTTTATTATTTCTTAAAAAAATATTCTTTTACC  
TGTCACCTGAATTTAGTAATGCCTTTTATGTTACACAACCTTAGCACTTTCCAGAAACAAAACTCTCTCCTTGAAA  
TAATAGAGTTTTTATCTACCAAAGATATGCTAGTGTCTCATTTCAAAGGCTGCTTTTTCCAGCTTACATTTTATAT  
ACTTACTCACTTGAAGTTTCTAAATATTCTTGTAATTTTAAACATATCTCAGATTTACTGAGGTTTATCTTCTGGT  
GGTAGATTATCCATAAGAAGAGTGATGTGCCAGAATCACTCTGGGATCCTTGCTGTGACAAGATTCAAAGGACTAAA  
TTAATTCAAGTCATGAACACTGCCAATTACCGTTTATGGGTAGACATCTTTGGAAATTTCCACAAGGTGAGACATT  
CGCAACTATCCCTTCTACATGTCCACACGTATACTCCAACACTTTATTAGGCATCTGATTAGTTTGGAAAGTATGC  
CTCCATCTGAATTAGTCCAGTGTGGCTTAGAGTTGGTACAACATTCTCACAGAATTTCTTAATTTTGTAGGTTTACG  
CCTGATAACCACTGGAGTTCTTTGGTCCTCATTAATAGCTTTCTTCACACATTGCTCTGCCTGTTACACATATGA  
TGAACACTGCTTTTTTAGACTTCATTAGGAATTTAGGACTGCATCTTGACAACCTGAGCCTATTCTACTATATGTAC



ATACCTAGCCCATAATAGGTATACAAATACACATTTGGTAAACTAATTTTCAACCAATGACATGTATTTTCAACT  
AGTAACCTAGAAATGTTTCACTTAAAATCTGAGAACTGGTTACACTACAAGTTACCTTGGAGATTCATATATGAAA  
ACGCAAACCTTAGCTATTTGATTGTATTCACTGGGACTTAAGAATGCGCCTGAATAATTGTGAGTTCGATTTGTTCT  
GGCAGGCTAATGACCATTTCAGTAAAGTGAATAGAGGTCAGAAGTCGTATAAAAGAGGTGTTGTCAGAACACCGT  
TGAGATTACATAGGTGAACAACATTTTTTAAGCAACTTTATTTGTGTAGTGACAAAGCATCCCAATGCAGGCTGAA  
ATGTTTCATCACATCTCTGGATCTCTCTATTTTGTGCAGACATTGAAAAAATTGTTTCATATTATTTCCATGTTATC  
AGAATATTTGATTTTTTAAAAACATAGGCCAAGTTCATTCACTTCATTATTTCATTTATCAAATCAGAGTGAATCA  
CATTAGTCGCCTTCACAACCTGATAAAGATCACTGAAGTCAAATTGATTTTTGCTATAATCTTCAATCTACCTATAT  
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GATTTTAGGTATCCTGTGAAAAGCAGAATTAAGACAAATACACAAGAGACAAAGCACAAAAATAAATATCATAAG  
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TTCACCTAGACAGCTTGGAGACAAGAAATTACCCAAAAGTAAGGTGAGGAGGATAGGCAAAAAGAGCAGAAAGATG  
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ATGAGGTAGGATGGGATAAACTCTTATTGAACCAATCTTCACCAATTTTGTTTTTCTTTTGCAGAGCAAGCTAGGA  
ATTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATAAAACAATTTG  
TATGGTATACACCTCCAACCTTTTATGATAGCTGTTTTCTTCCAATTGTTGTCCTGATATTTAAAAGCATACTATT  
CCTGCCATGCTTGAGGAAGAAGATACTGAAGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACCTGAG  
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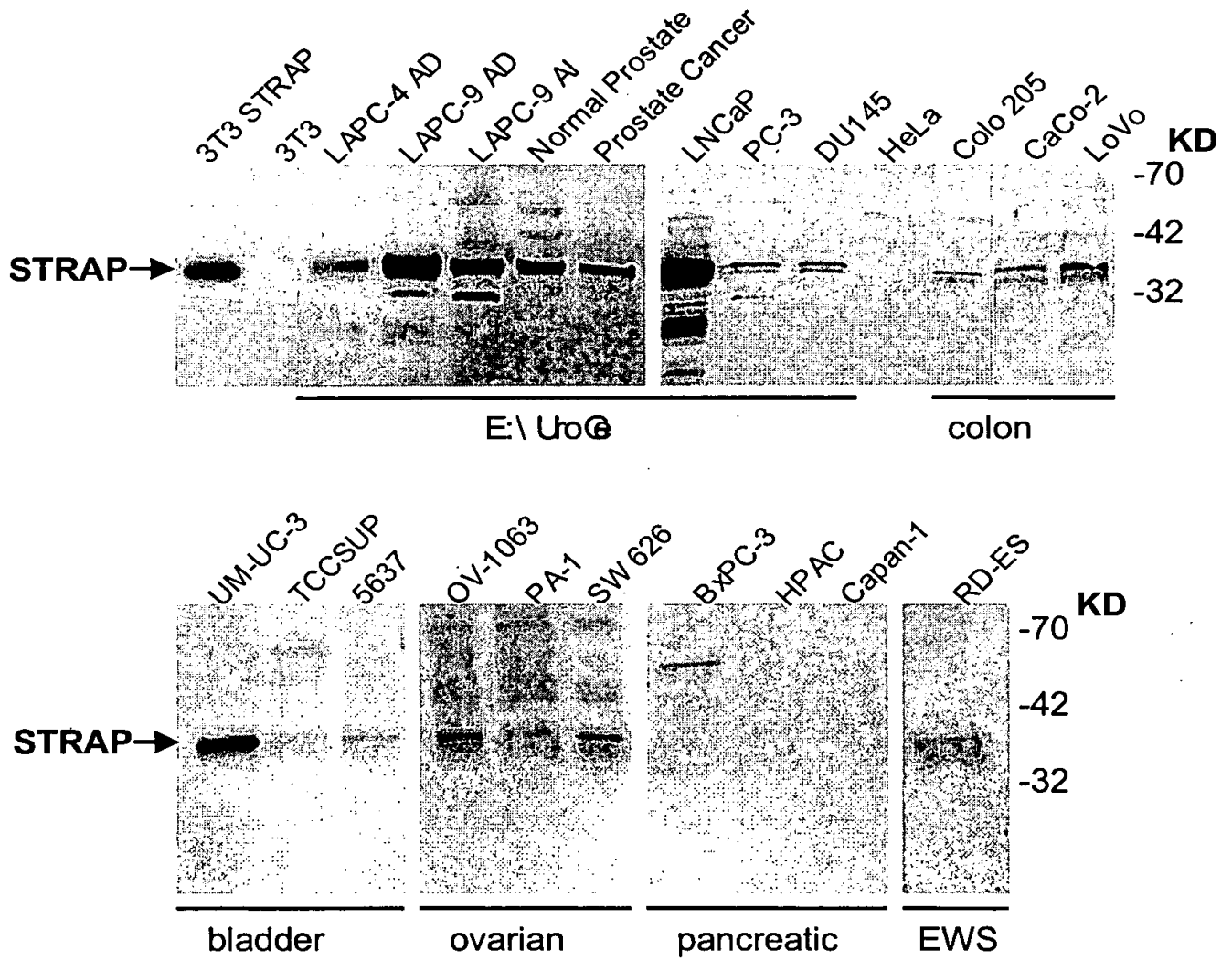
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FIG. 5



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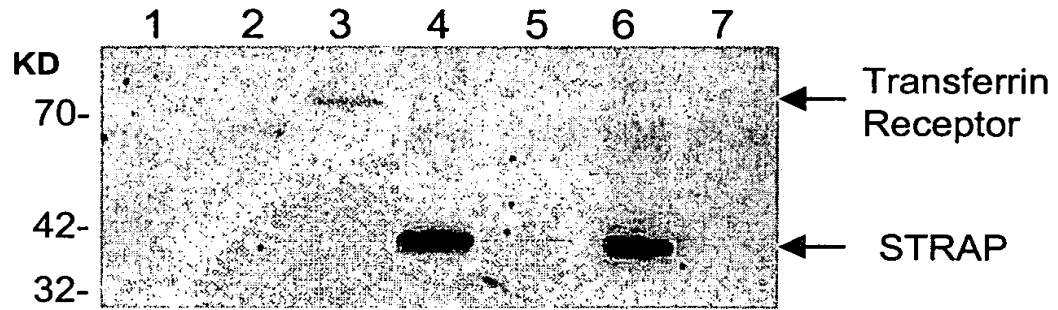
**FIG. 6**



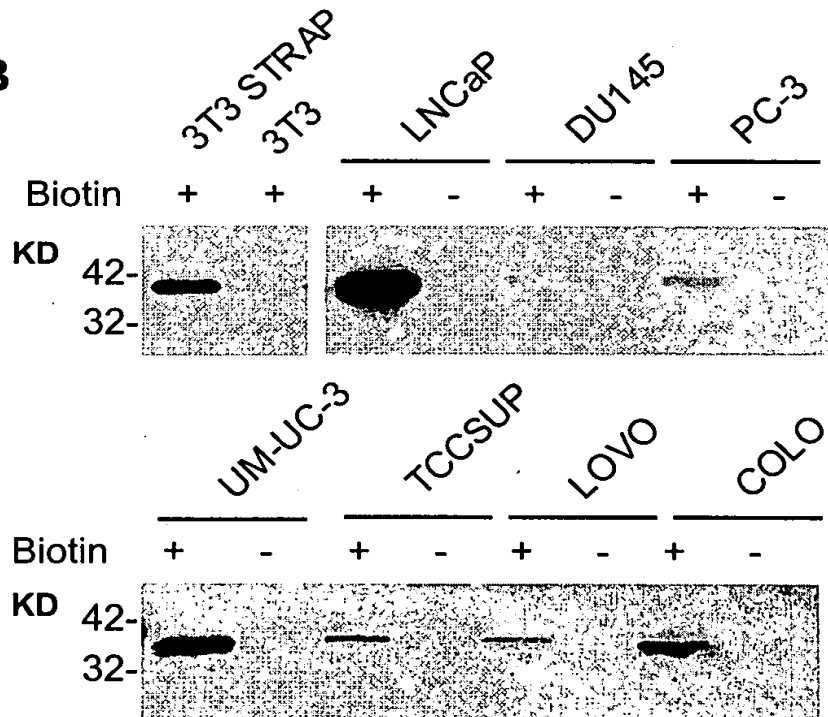
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# FIG. 7

**A**

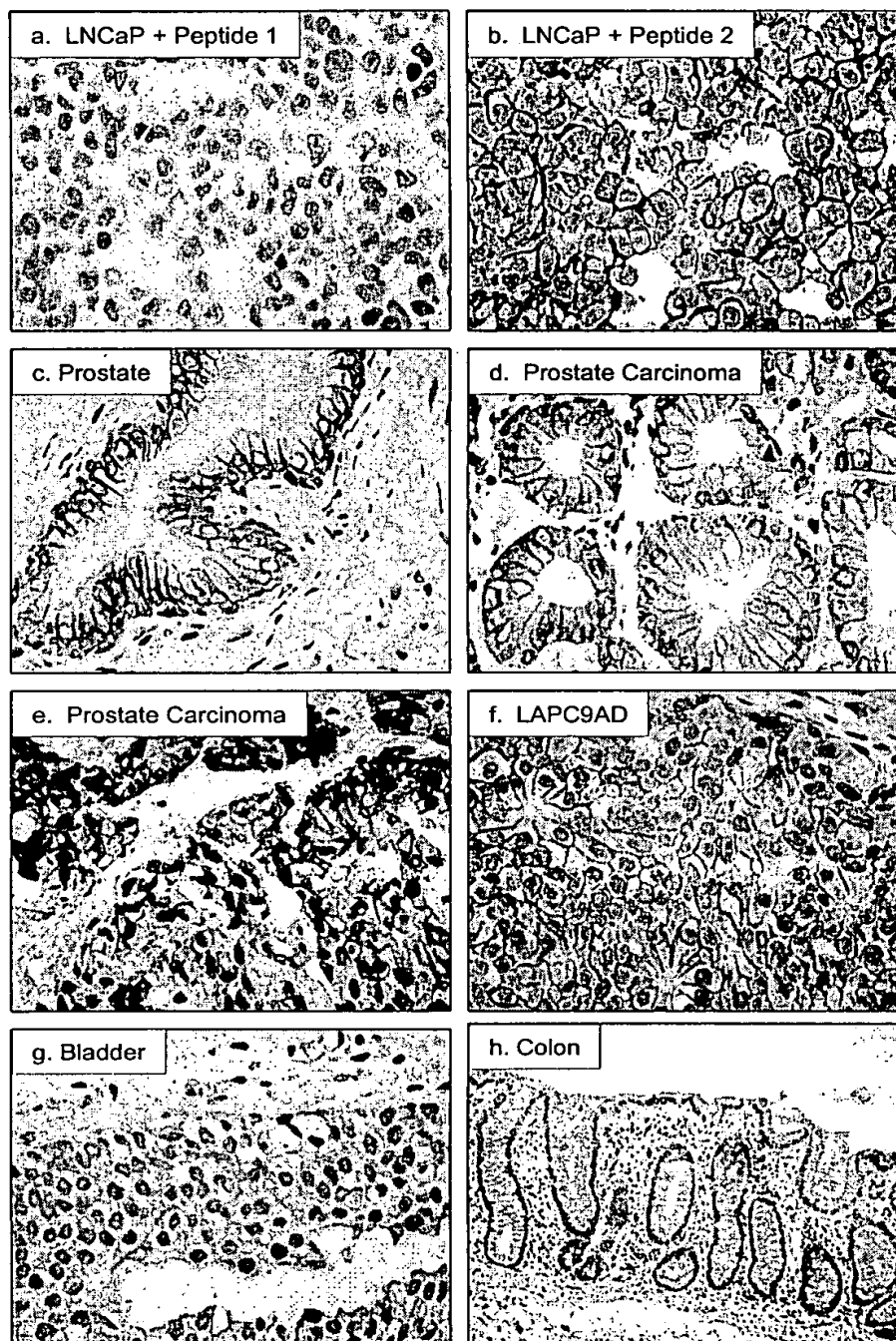


**B**



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FIG. 8



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# FIG. 9

```

5'   10      19      28      37      46      55
    GAC TTT TAC AAA ATT CCT ATA GAG ATT GTG AAT AAA ACC TTA CCT ATA GTT GCC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Asp Phe Tyr Lys Ile Pro Ile Glu Ile Val Asn Lys Thr Leu Pro Ile Val Ala

      64      73      82      91     100     109
    ATT ACT TTG CTC TCC CTA GTA TAC CTC GCA GGT CTT CTG GCA GCT GCT TAT CAA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Ile Thr Leu Leu Ser Leu Val Tyr Leu Ala Gly Leu Leu Ala Ala Ala Tyr Gln

      118     127     136     145     154     163
    CTT TAT TAC GGC ACC AAG TAT AGG AGA TTT CCA CCT TGG TTG GAA ACC TGG TTA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Leu Tyr Tyr Gly Thr Lys Tyr Arg Arg Phe Pro Pro Trp Leu Glu Thr Trp Leu

      172     181     190     199     208     217
    CAG TGT AGA AAA CAG CTT GGA TTA CTA AGT TTT TTC TTC GCT ATG GTC CAT GTT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Gln Cys Arg Lys Gln Leu Gly Leu Leu Ser Phe Phe Phe Ala Met Val His Val

      226     235     244     253     262     271
    GCC TAC AGC CTC TGC TTA CCG ATG AGA AGG TCA GAG AGA TAT TTG TTT CTC AAC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Ala Tyr Ser Leu Cys Leu Pro Met Arg Arg Ser Glu Arg Tyr Leu Phe Leu Asn

      280     289     298     307     316     325
    ATG GCT TAT CAG CAG GTT CAT GCA AAT ATT GAA AAC TCT TGG AAT GAG GAA GAA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Met Ala Tyr Gln Gln Val His Ala Asn Ile Glu Asn Ser Trp Asn Glu Glu Glu

      334     343     352     361     370     379
    GTT TGG AGA ATT GAA ATG TAT ATC TCC TTT GGC ATA ATG AGC CTT GGC TTA CTT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Val Trp Arg Ile Glu Met Tyr Ile Ser Phe Gly Ile Met Ser Leu Gly Leu Leu

      388     397     406     415     424     433
    TCC CTC CTG GCA GTC ACT TCT ATC CCT TCA GTG AGC AAT GCT TTA AAC TGG AGA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Ser Leu Leu Ala Val Thr Ser Ile Pro Ser Val Ser Asn Ala Leu Asn Trp Arg

      442     451     460     469     478     487
    GAA TTC AGT TTT ATT CAG TCT ACA CTT GGA TAT GTC GCT CTG CTC ATA AGT ACT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Glu Phe Ser Phe Ile Gln Ser Thr Leu Gly Tyr Val Ala Leu Leu Ile Ser Thr

      496     505     514
    TTC CAT GTT TTA ATT TAT GGA TGG AAA CGA GCT 3'
    --- --- --- --- --- --- --- --- --- ---
    Phe His Val Leu Ile Tyr Gly Trp Lys Arg Ala

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# FIG. 10

STRAP-2, AA508880 (NCI\_CGAP Pr6)

ggtcgacttttccctttattcctttgtcagagatctgattcatccatattgctagaaaccaacagagtgaacttttaca  
aaattcctatatagagattgtgaataaaaaccttacctatagttgccattactttgctctccctagtataccttgcagg  
tcttctggcagctgcttatcaactttattacggcaccaagtataggagatttccaccttgggtggaaacctgggta  
cagtgtagaaaacagcttgattactaagttgtttcttcgctatgggccatgttgccctacagcctctgcttaccga  
tgagaaggtcagagagat

STRAP-2, 98P4B6 SSH fragment

TTTGACGCTTTGCAGATACCCAGACTGAGCTGGAAGTGAATTTGTCTTCCTATTGACTCTACTTCTTTAAAGCG  
GCTGCCCATTACATTCCCTCAGCTGTCCTTGCAAGTTAGGTGTACATGTGACTGAGTGTGGCCAGTGAGATGAAGTC  
TCCTCAAAGGAAGGCAGCATGTGTCCTTTTT

AI139607 (testis EST)

aagaaggagaatccatttagcacctcctcagcctggctcagtgattcatatgtggctttgggaataacttggggttt  
ttctgtttgtactccttgggaatcacttctttgccatctgttagcaatgcagtcactggagagagttccgatttgt  
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acactagaaaaagcattgaatggaaaatcaatatttaaaacaaagttcaatttagctggaaaaaaaaa

R80991 (placental EST)

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# FIG. 11A

```
STRAP-1 106 FYKIPILVINKVLPMSITLLALVYLPGVIAAIVQLHNGTKYKKFPHWLDKWMLTRKQFG
STRAP-2 2 FYKIPIEIVNKTLPPIVAITLLSLVYLAGLLAAAYQLYYGTKYRRFPPWLETWLQCRKQLG
          ***** ** * * * * * * * * * * * * * * * * * * * * * * * * * * * *

STRAP-1 166 LLSFFFAVLHAIYSLSPMRRSYRYKLLNWAYQQVQONKEDAWIEHDVVRMEIYVSLGIV
STRAP-2 62 LLSFFFAMVHVAYSLCLPMRRSERYLFLNMAYQQVHANIENSWNEEEVWRIEMYISFGIM
          ***** * * * * * * * * * * * * * * * * * * * * * * * * * * * *

STRAP-1 226 GLAILALLAVTSIPSVSDSLTWREFHYIQSKLGIVSLLGTIHALIFAWNK
STRAP-2 122 SLGLLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYGWKR
          * * * * * * * * * * * * * * * * * * * * * * * * * * * *
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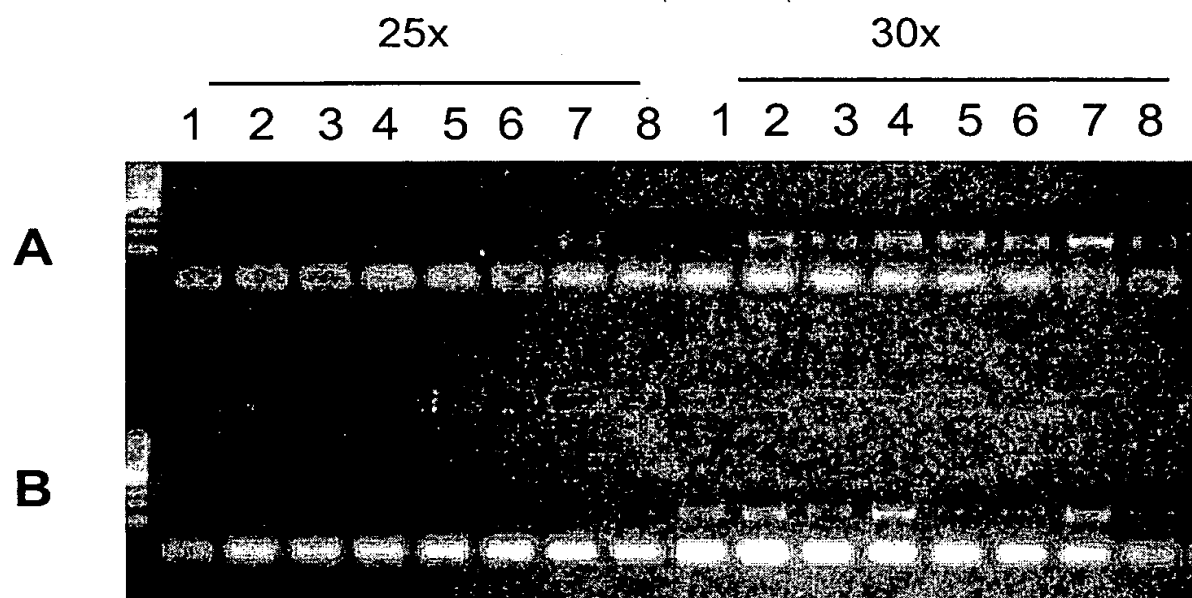
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FIG. 11B

1	15 16	30 31	45 46	60 61	75 76	90
STRAP-1	MESRKDITNOEELWK	MKPRRNLEEDDYLHK	DTGETSMLKRPVLLH	LHQTAAHDEFDCPSE	LQHTQELFPQWHLPI	KIAAIIASLTFLYTL
STRAP-2	-----	-----	-----	-----	-----	-----
STRAP-3	-----	-----	-----	-----	-----	-----
STRAP-4	-----	-----	-----	-----	-----	-----
91	105 106	120 121	135 136	150 151	165 166	180
STRAP-1	LREVIHPLATSHQQY	FYKIPILVINKVLPM	VSITLLALVILPGVI	AAIVQLHNGTKYKKF	PHWLDKMWMLTRKQFG	LLSFFFAVLHAYTSL
STRAP-2	-----D	FYKIPILVINKVLPI	VAITLLSLVILAGGL	AAAYQLYYGTYKRRF	PPWDETWLQCRKQUG	LLSFFFAVAVAYTSL
STRAP-3	-----	-----	-----	-----	-----	-----
STRAP-4	-----	-----	-----	-----	-----	-----
181	195 196	210 211	225 226	240 241	255 256	270
STRAP-1	SYPMRRSRVRYKLLNW	AYQOVQONKEDAWIE	HDVWRMEIYVSLGIV	GLAILALGLAVTSIPS	VSDSLTWREFHVIQS	KLGIVSLDGLQTHAL
STRAP-2	CIPMRRSRERYLFLNW	AYQOVHANIEHSWNE	EEVWRIEMYISFGIM	SLGLLSLLAVTSIPS	VSNALNWREFSFVQS	TLCGYVALLGISTFHVIL
STRAP-3	-----	-----	-----	-----	-----	-----
STRAP-4	-----ATTWSTW	QSSRSWPXKSHLWVK	EEVWRMEIYLSIGVII	ALGTLSSLAVTSIPS	IANSINWREFSFVQS	SLGTFVAXVLSLTLHTIL
271	285 286	300 301	315 316	330 331	345 346	360
STRAP-1	IFAWNKWIDIKQFVW	YTPPTFMIAVFLPIV	VLLIFKSLFLPCLTRK	KILKIRHGWEDVTKI	NKTEICSQL	339
STRAP-2	YGWKRA	-----	-----	-----	-----	173
STRAP-3	VYGGKRFSLSPSNLRW	YLPAAVILGLIIPCT	VLVIRFVLIMPCVDN	TLIRIQGWERNKSH	-----	128
STRAP-4	TYGWTRAPEESRYKF	YLPPTFTXTLLVPCV	RSSWAKALEFLPCIQ	P-----	-----	128

# FIG. 12



**A**

**B**

**A**

1. Brain
2. Heart
3. Kidney
4. Liver
5. Lung
6. Pancreas
7. Placenta
8. Skeletal Muscle

**B**

1. Colon
2. Ovary
3. Leukocytes
4. Prostate
5. Small Intestine
6. Spleen
7. Testis
8. Thymus

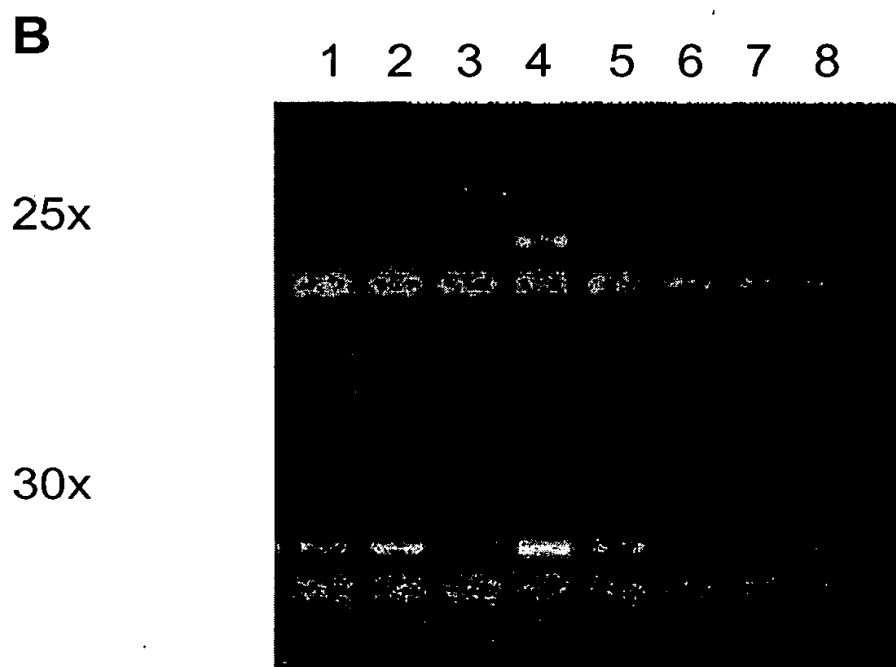
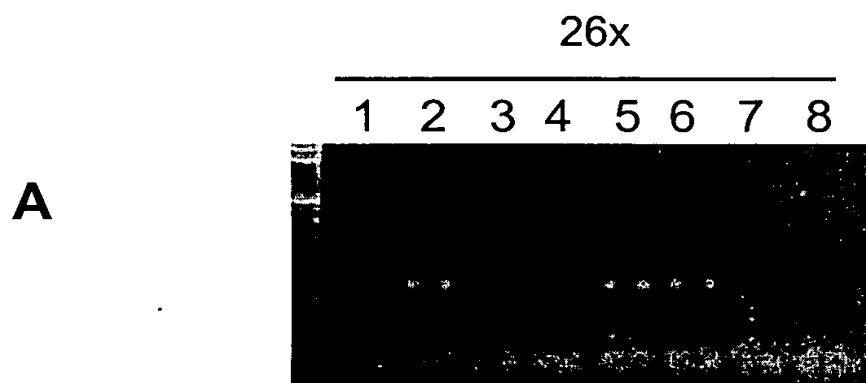
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**B**

1. Colon
2. Ovary
3. Leukocytes
4. Prostate
5. Small Intestine
6. Spleen
7. Testis
8. Thymus

# FIG.14



- A**
1. Brain
  2. Prostate
  3. LAPC-4 AD
  4. LAPC-4 AI
  5. LAPC-9 AD
  6. HeLa
  7. Murine cDNA
  8. Neg. control

- B**
1. Colon
  2. Ovary
  3. Leukocytes
  4. Prostate
  5. Small Intestine
  6. Spleen
  7. Testis
  8. Thymus

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FIG. 15

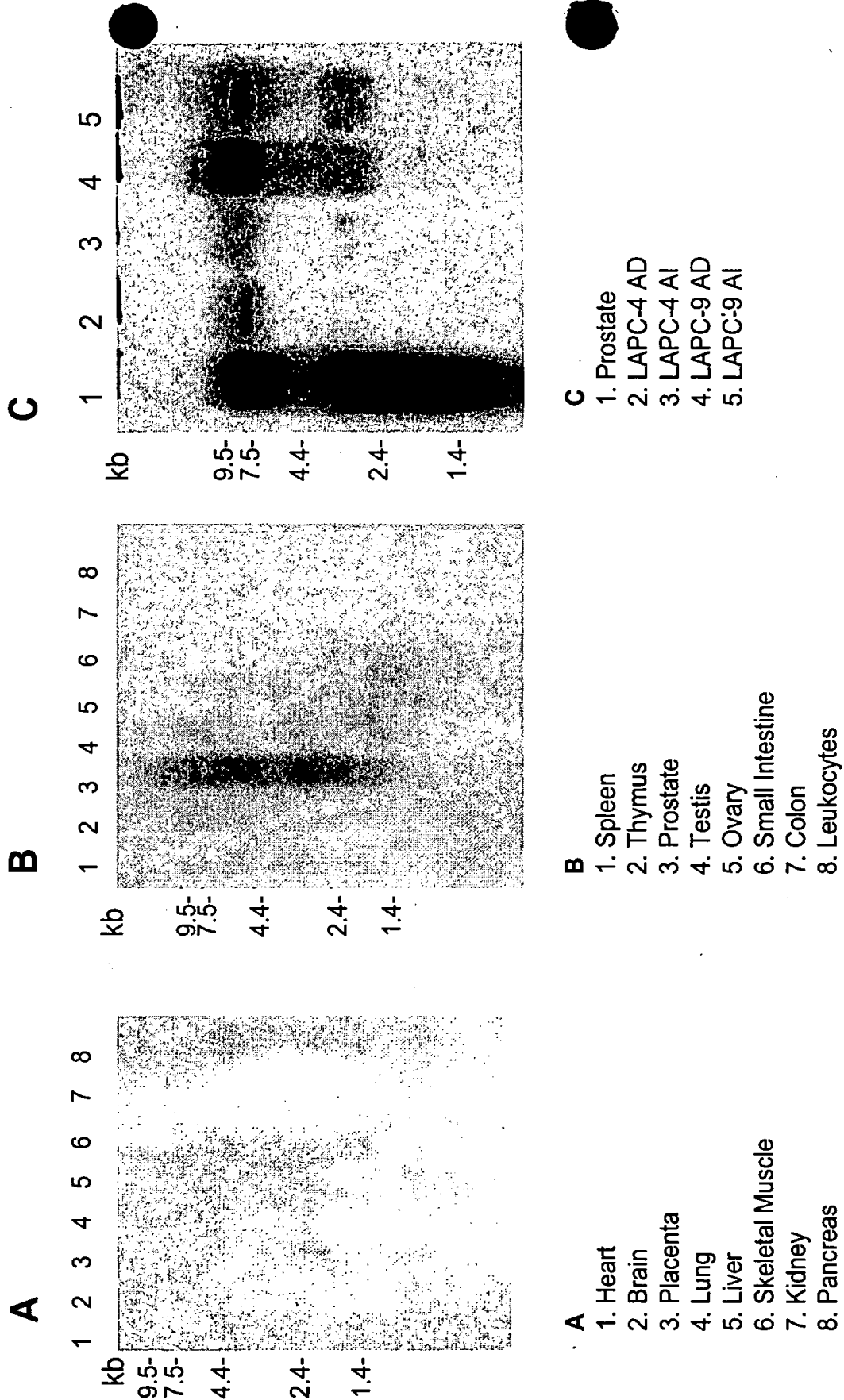
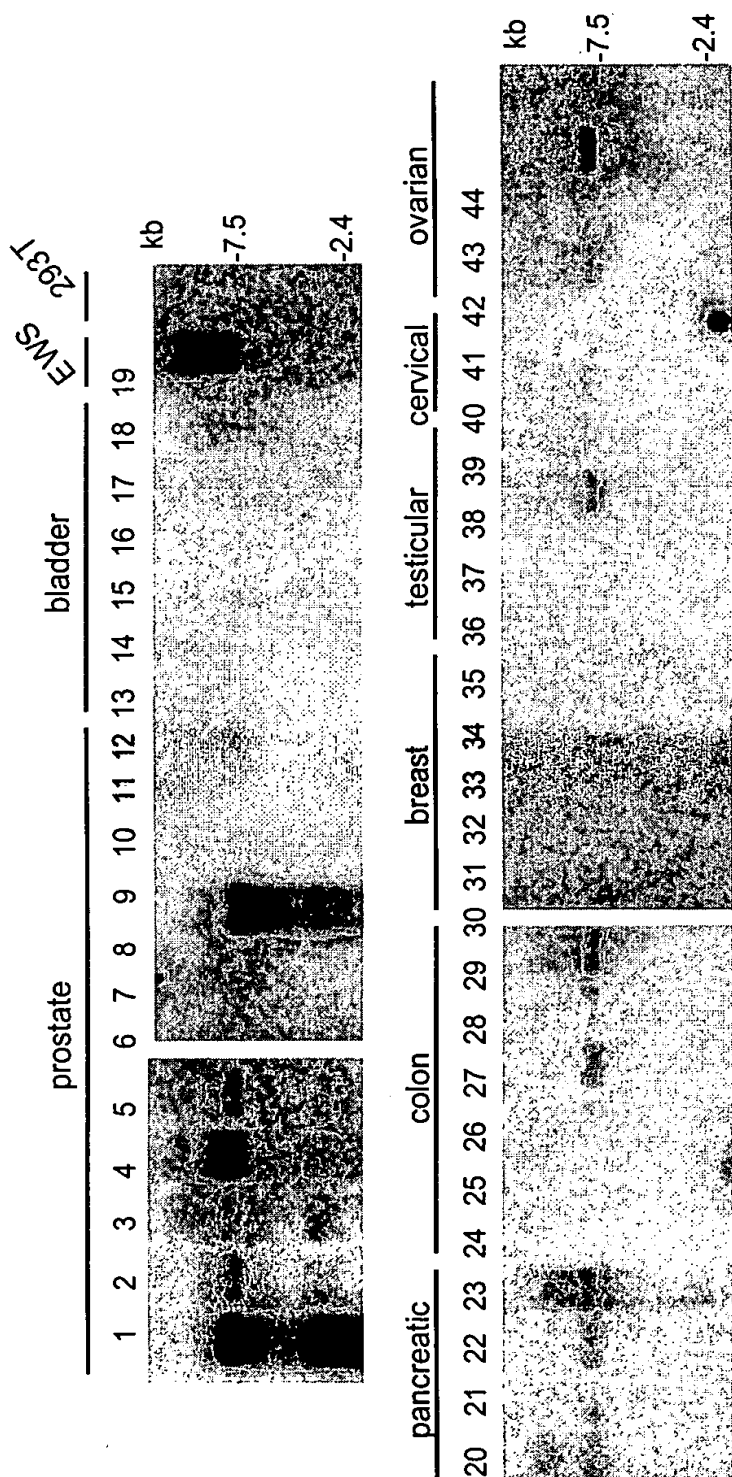


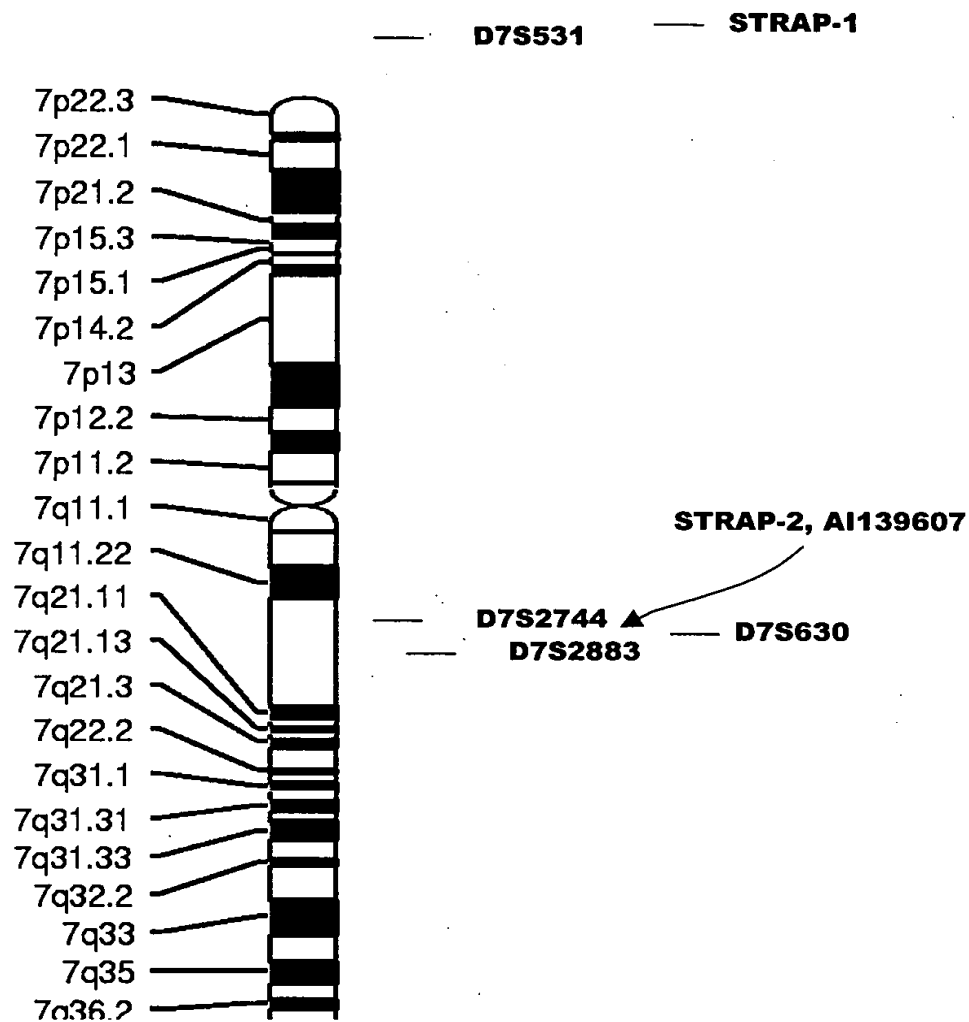
FIG. 16



- |               |             |              |                 |             |
|---------------|-------------|--------------|-----------------|-------------|
| 1. prostate   | 12. HT1197  | 20. PANC-1   | 30. BT-20       | 39. A431    |
| 2. LAPC-4 AD  | 13. SCaBER  | 21. BxPC-3   | 31. CAMA-1      | 40. HeLa    |
| 3. LAPC-4 AI  | 14. UM-UC-3 | 22. HPAC     | 32. DU4475      | 41. OV-1063 |
| 4. LAPC-9 AD  | 15. TCCSUP  | 23. Capan-1  | 33. MCF-7       | 42. PA-1    |
| 5. LAPC-9 AI  | 16. J82     | 24. LS180    | 34. MDA-MB-435s | 43. SW626   |
| 6. TsuPr1     | 17. 5637    | 25. SK-CO-1  | 35. NTERA-2     | 44. CAO-V-3 |
| 7. DU145      | 18. RD-ES   | 26. CaCo-2   | 36. NCCIT       |             |
| 8. LNCaP      | 19. 293T    | 27. LoVo     | 37. TERA-1      |             |
| 9. PC-3       |             | 28. T84      | 38. TERA-2      |             |
| 10. LAPC-4 CL |             | 29. Colo-205 |                 |             |
| 11. PrEC      |             |              |                 |             |

# FIG. 17

## GDB Compreher



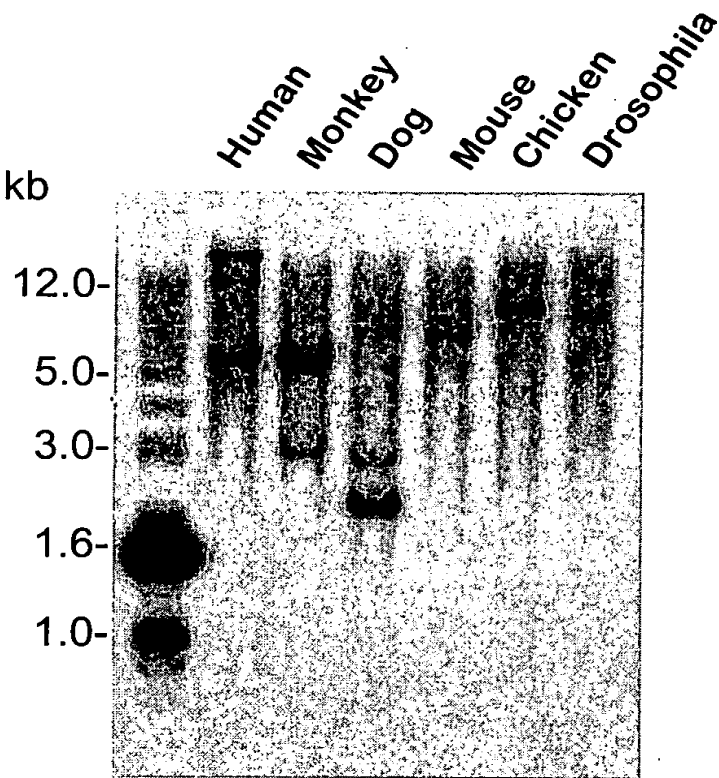
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FIG. 18

-31	84	85	597	598	762	763	1177
	i						
	e		e		e		e

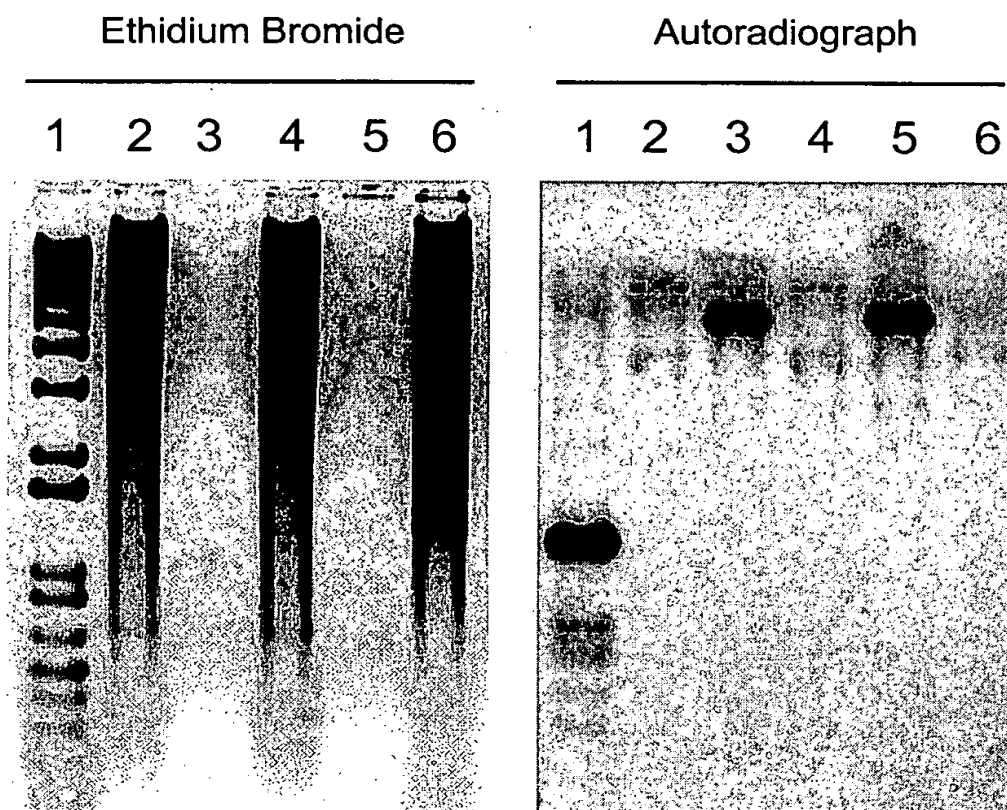


FIG. 19



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**FIG. 20**



**Lanes**

- 1) 1kb ladder
- 2) human female genomic
- 3) 12P11 BAC mus
- 4) human female genomic
- 5) 12P11 BAC mus
- 6) 3T3